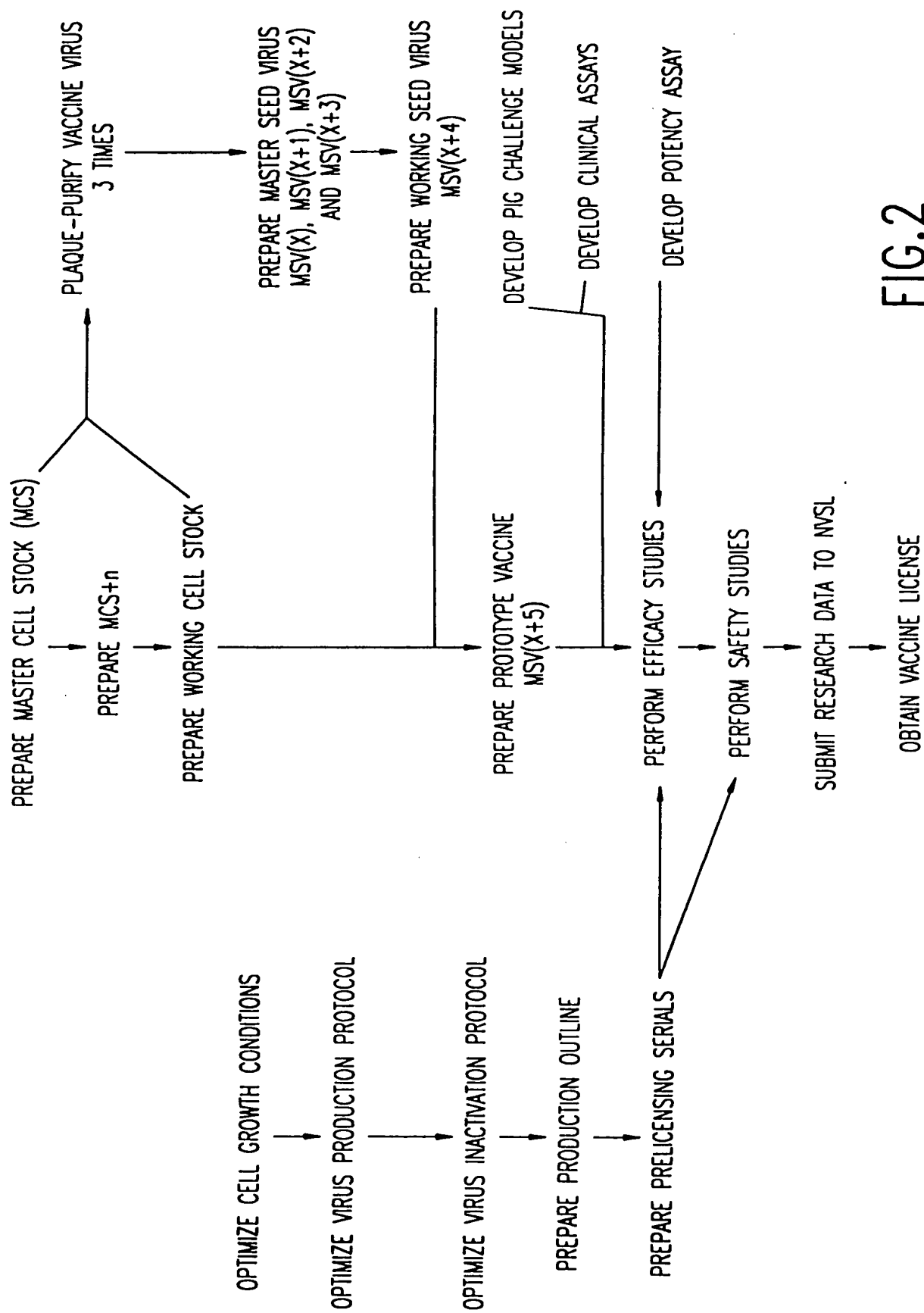


FIG.1



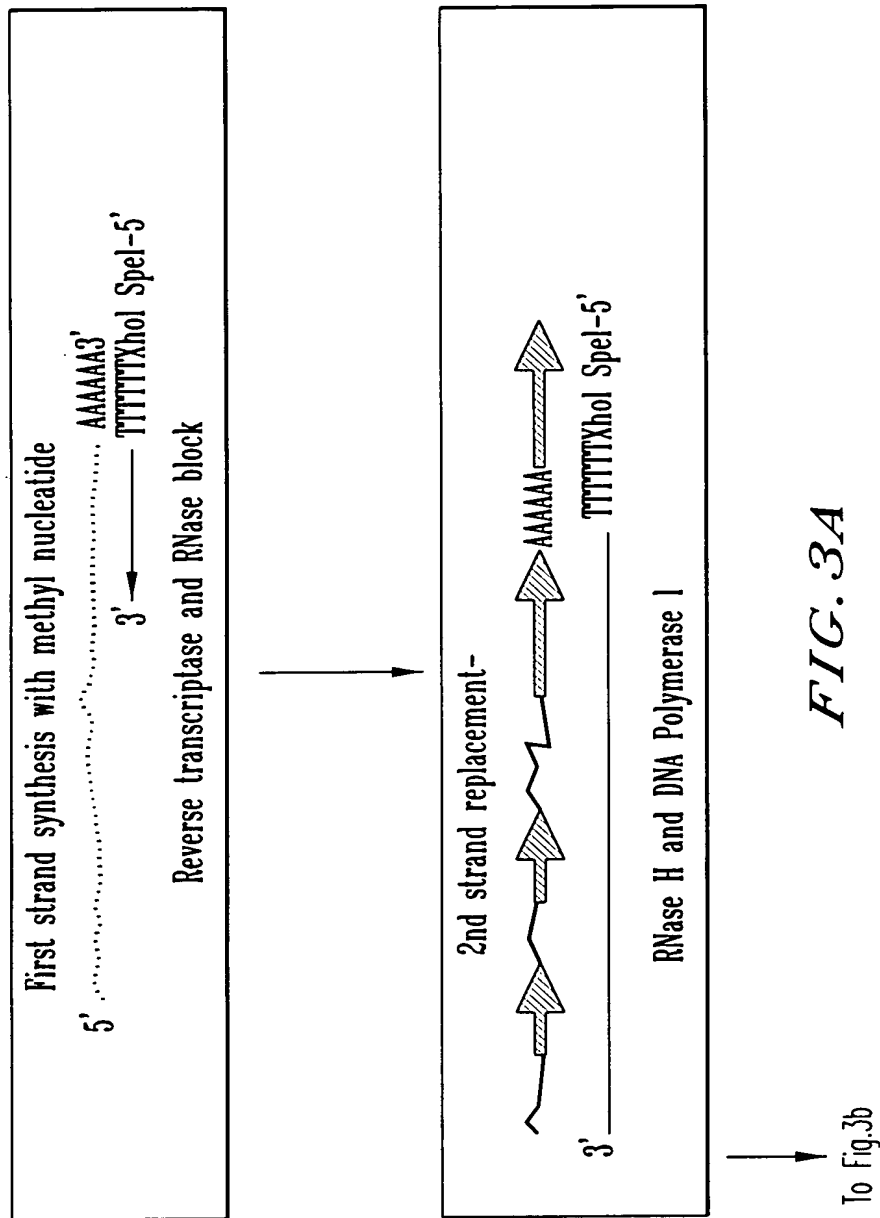


FIG. 3A

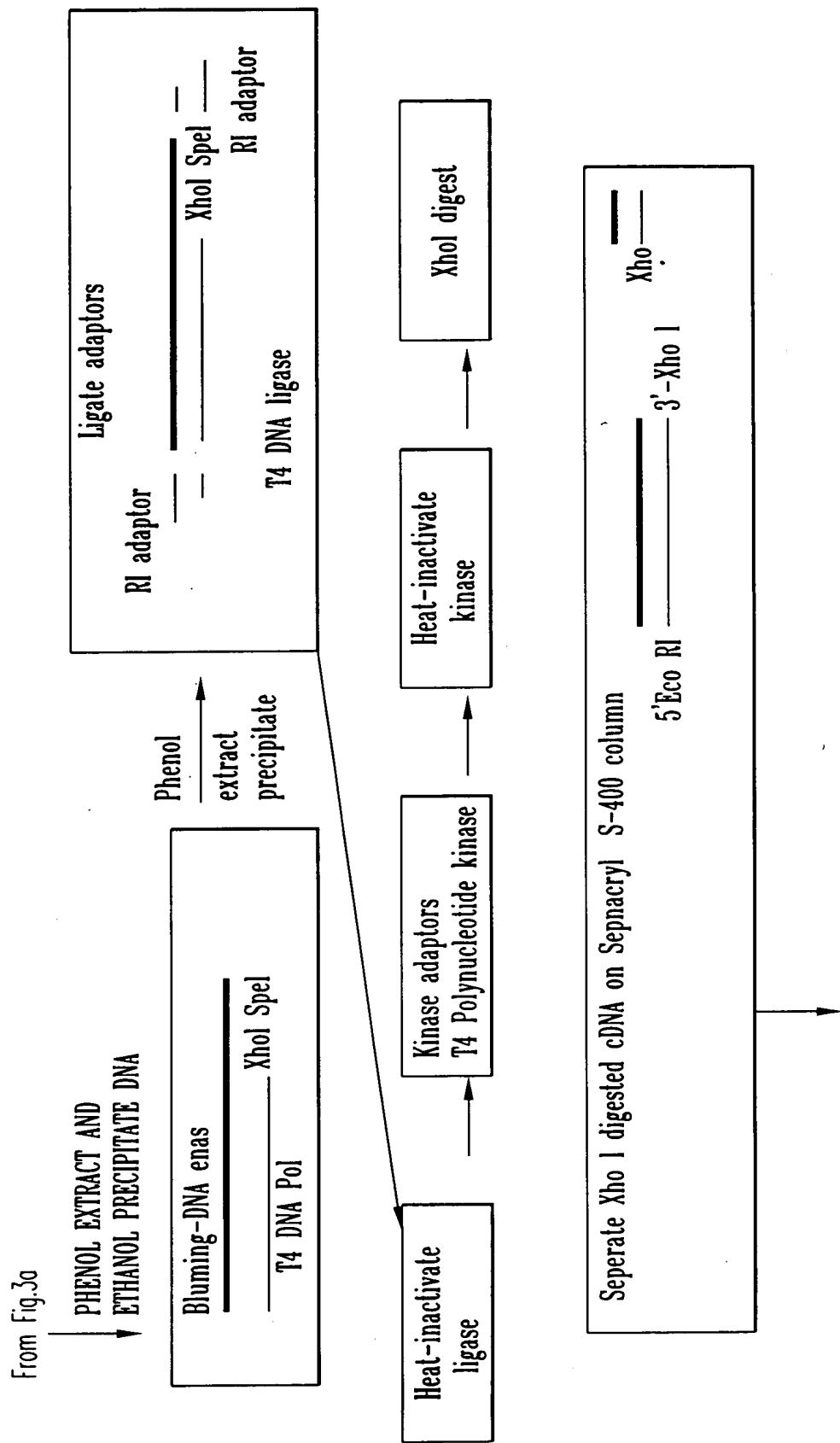


FIG. 3B

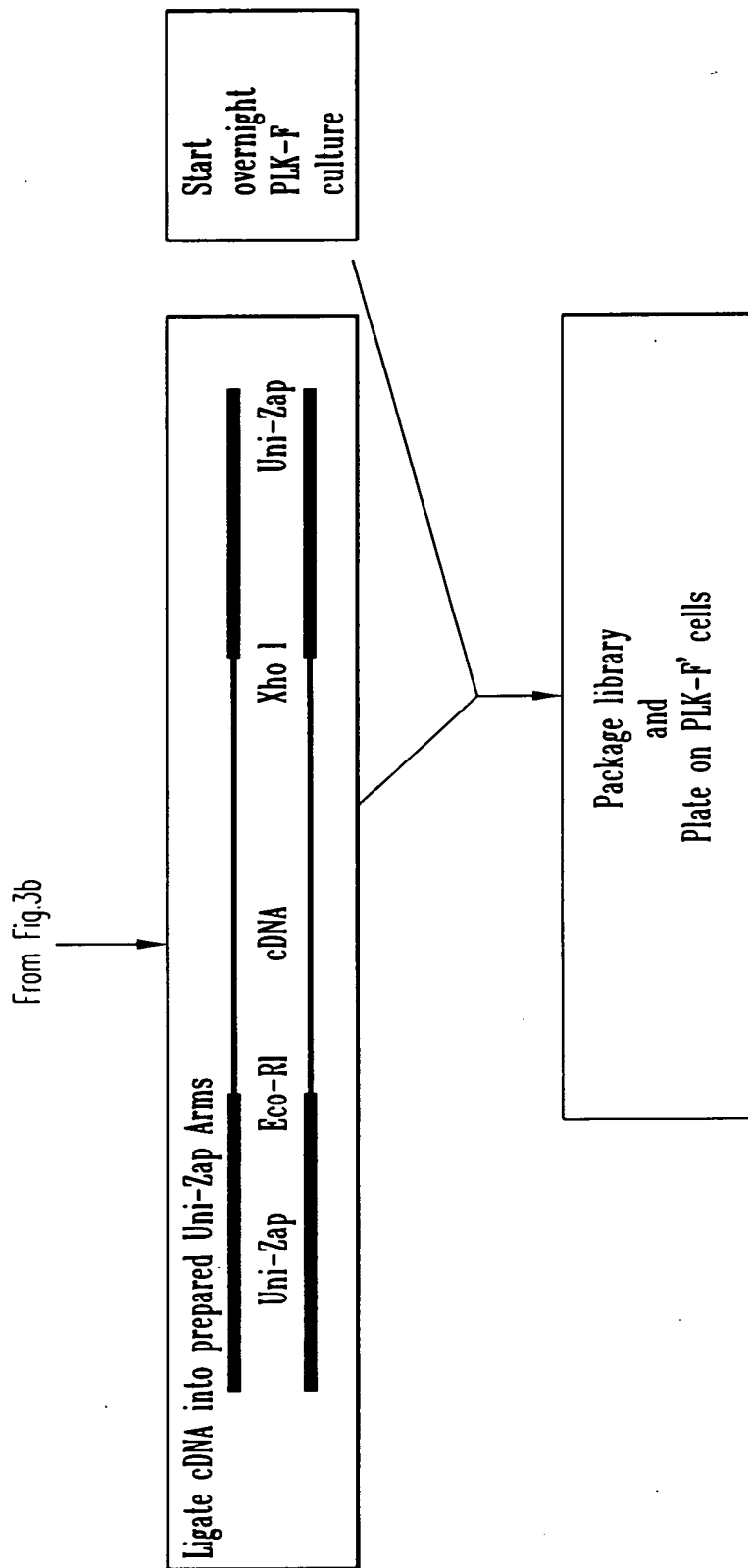


FIG. 3c

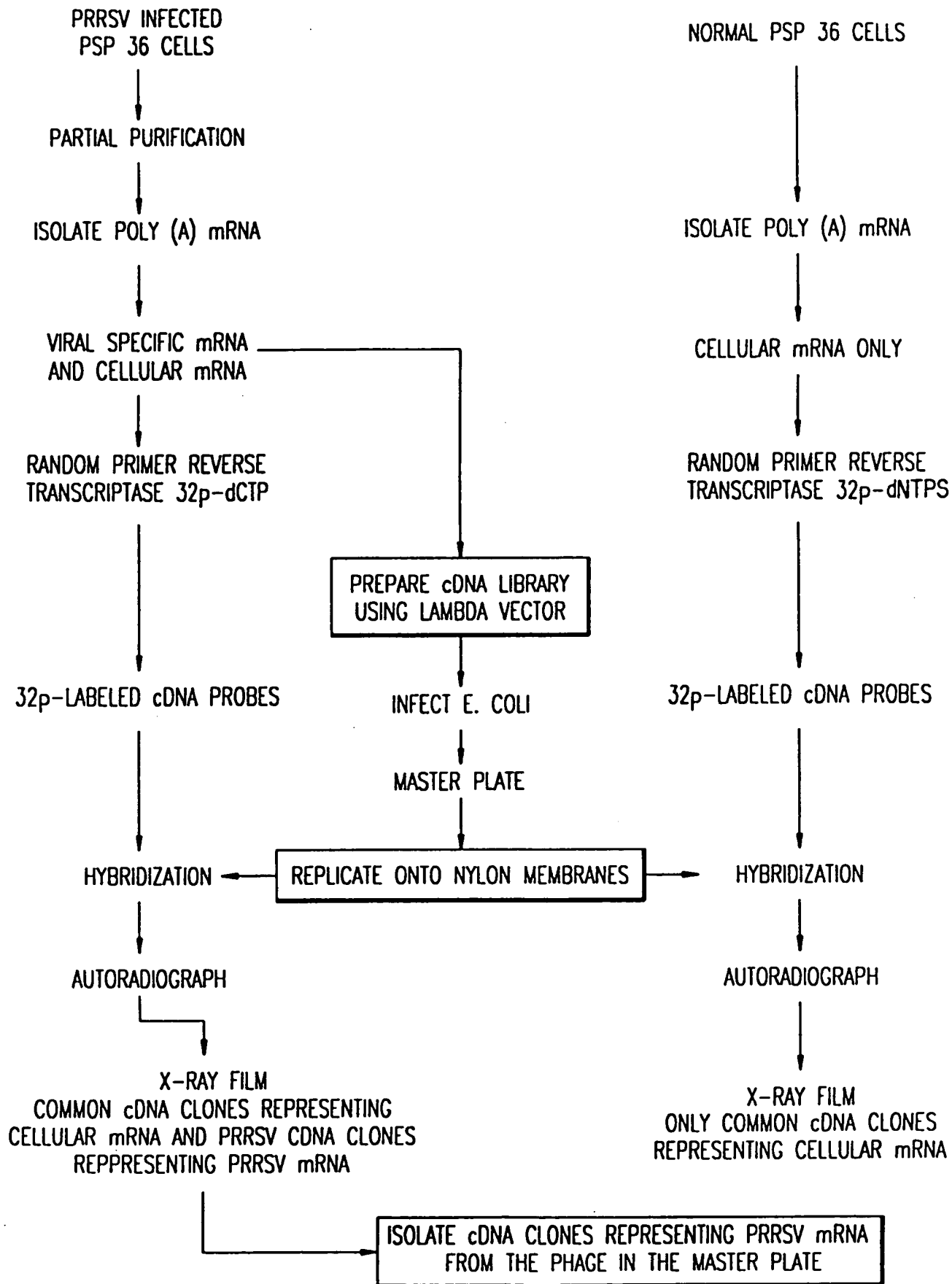


FIG.4

FOOTED TOSOTBOD

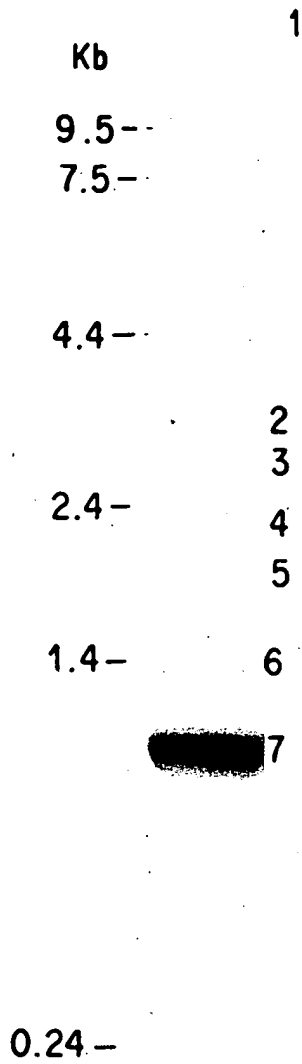


FIG.5

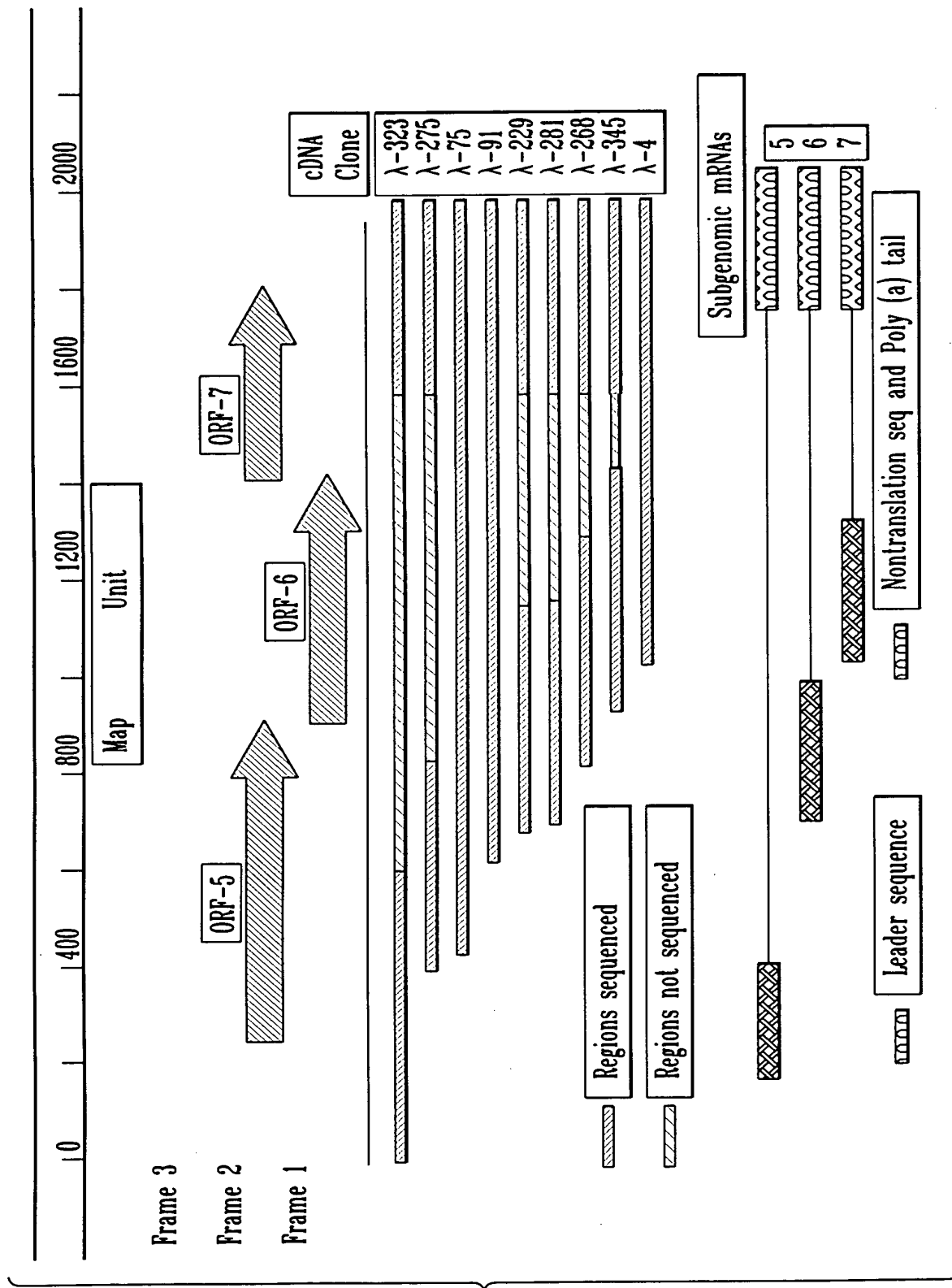


FIG. 6



GGCAGGCTTGGTGTCTCCAAAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCTAGGGGATTCCGAAAGTCCCTCAGTCCGCGACGGCGATAGGG 100  
 ACACCCGTGTATACACTGTCACAGCCCAATGTTACCGATGAGAAATTATTGCAATCCCTGATCTTCATGCTTCTTGGCTTTTCTAIGCTTCTG 200  
 AGATGAGTGAAAGGGATTTAAGGTGGTATTGGCAATGCTCAGGCATCGTGGCAGTGTGGCTCAACTTACCAGTTACGTCCAACATGTCAGGGAATT 300  
 TACCCAACGTTCCTTGGTAGTTGACCATGTGGGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCAACTGTTTAGCCTGCTTTTTTGGCATT 400  
 DRF 4 stop  
 \*\*\* +1>DRF5 start  
 CTGTTGGCAATTGAA TGTTAAGTATGTTGGGAAATGCTTGACCGGGGCTGTTGCTCGCAATTGCTTTTTTTGGTGTATCGTCCGCTTGTTTT 500  
 GTTGGCTGTCAGCGCCACGGGAACAGCGGCTCAAAATTACAGCTGATTTACAAC TTGACGCTATGTGAGCTGAATGGCACAGATTGGCTAGCTAATA 600  
 AATTTGACTGGGCAGTGGAGTGTTTTGTCAATTTTCCTGTTGACTCACATTGTCTCTTATGGTGGCTCAC TACTAGCCATTTCCTTGACACAGTCGG 700  
 TCTGGTCACTGTCTACCGCTGGGTTTGTTCACGGGGGTA GTTCTGAGTAGCATGTACGGGGTCTGCGCC TGGCTGGCTTGATTGGCTTCGTCATT 800  
 AGGCTTCCGAGAATTGCA TGTCCTGGCGTACTCATGTACCAGATATACCAACTTCTCTGGACACTAAGGGCAGACTCTATCGTTGGCGGTGCGCTG 900  
 TCATCATAGAGAAAGGGCAAGTTGAGGTGGAAGGTCACCTGATCGACCTCAAAAGAGTTGTGCTTGATGGTTCCGCGGCTACCCCTGTACCCAGAGT 1000  
 DRF6 start  
 +1> \*\*\*DRF5 stop  
 TTCAGCGGAACAATGGAGTCGTCCTTAGATGACTTCTGTCA TGATAGCAGGCTCCACAAAGGTGCTCTTGGCGTTTCTATTACCTACACGCCAGTGA 1100

FIG. 7A

TGATATATGCCCTAAAGGTGAGTCGCGGCCGACTGCTAGGGCTTCCTGCACCTTTTGGGCTCCCGAATTGTGCTTTCACCTTCGGGTACATGACATTGGT 1200  
 GCACCTTCAGAGTACAAATAAGGTGCGGCTCAGTATAGGAGCAGTAGTTGCACCTCTTTGGGGGGGTGCTACTAGCCATAGAAACCTGGAAATTCATCACC 1300  
 TCCAGATGCCGTTTGTGCTTGTAGGCGCGAAGTACATTCTGGCCCTGCCACCACAGTTGAAGTGC CGAGGCTTTCATCCGATTGCGGCAAAATGATA 1400  
 ACCACGCCATTTGTGTCGCGGCTCCCGGCTCCACTACGGTCAACGGCACATTGGTCCCCGGTTAAAGGCTCGTGTGGGTGGCAGAAAGCTGTTAA 1500  
 ACCAGGGAGTGGTAAACCTTGTTAATATGCCAAATAACACCGGCAAGCAGCAGAGAGAAAGGGGATGGCCAGCCAGTCAATCAGCTGTGCCAGAT 1600  
 GCTGGGTAGATCATCGCTCACCAAAACCACTCCAGAGGCAAGGGACCGGGAAGAAAAAATAAGAAAGAAACCCGGAGAGCCCCCATTTCCCTCTAGCG 1700  
 ACTGAAGATGATGTCAGACATCACTTACCCCTAGTGAGCGTCAATTGTGCTGCTCAATCCAGACCGGCTTAAATCAAGGCGCTGGGACTTGCACCC 1800  
 TGTGAGATTCAGGGAGGATAAGTTACACTGTGGAGTTAGTTGGCTACGCATCATACTGTGGCGCTGATCCGGCTCACAGCATCACCCTCAGCATGATG 1900  
 GGTGGCATTCCTGAGGCATCCAGTGTGTGAATTGGAAGATGCGTGGTGAATGGCAGTGAATTGACATTTGTGCTCTAAGTCACCTATTCAATTAGGGC 2000  
 GACCGTGTGGGGTAAGATTTAATTGGCGAGAACACACGGCGGAAATTAATAAAAAAAAAA 2062

DRF7 start

+1> \*\*\*DRF6 stop

\*\*\*DRF7 stop

FIG. 7B

LELYSTAD SEQ (13484-14089)	ATGAGATGTTCTCACAAATGGGGCGTTTCTTGACGCCACCTCTTGCCTCTGGTGGCTTTTTTCTCTGTGTA--	13556
ISU-12-3' TERMINAL (426-1028)	-----ATGTTGGGGAAATGCTTGACCGCGCTTGTGCTGCAATTTGCIIIIIIITGGTGATC	485
LELYSTAD SEQ (13484-14089)	---CCGCTTGTCTGTT-CTTTTCCGATGTCACGGCCACAGGTCGACATACCAATA-C-ATATATAACTTG	13624
ISU-12-3' TERMINAL (426-1028)	GTCCGCTCTTGTTTCTTGGGCTCTCAGCCCAACGGACACGGGCTCAATTTACAGCTGATTTACAACTTG	560
LELYSTAD SEQ (13484-14089)	ACGATATGGAGCTGAATGGGACCTGCTGTTGTTCCAGCCATTTTGTGTTGGGCACTGAGACCTTTGTGCTTAC	13699
ISU-12-3' TERMINAL (426-1028)	ACGCTATGTTGAGCTGAATGGGACAGATTTGGCTAGGTAATATATATTTGACTGGGCACTGAGTGTTTTGTCAATTTT	635
LELYSTAD SEQ (13484-14089)	CCGTTGCCACTCATATCCCTCTCACTGGGTTTCTCACAAAGGCCATTTTGTGACCTGGCTCTGGGCT	13774
ISU-12-3' TERMINAL (426-1028)	CGTGTGTTGACTCACATGTTCTCTTATGTTGGTCCCTCAGTACTAGGCCATTTCTTGACACAGTGGGCTCTGGTACT	710
LELYSTAD SEQ (13484-14089)	GTAATCCACTGCAAGATTGTTGTTGGCGGGCGGTAGTACTCTCCAGCTCTACGGCTTTGTGCTTTCCGACGGCTTC	13849
ISU-12-3' TERMINAL (426-1028)	GTGTCTACCGCTGGTTTGTTCACGGGCGGTATGTTCTGAGTAGCATGTACCGCTCTGTGTCCTTGGCTGGCTTG	785
LELYSTAD SEQ (13484-14089)	GTATGTTTGTGTCATCCGTGCTGTAAATAATTGATGCTCCGCTATGCTCGTACCGCTTTACCAACTTCATT	13924
ISU-12-3' TERMINAL (426-1028)	AATTTGCTTGTCAATAGGCTTGGCAAGCAATTGCAATGCTCTGGCTACTCATGTACCAAGATATACCAACTTTCTT	860
LELYSTAD SEQ (13484-14089)	GTGGACGACCGGGGAGAGTTTCATCGATGGAAGTCTCCAAATAGTGGTAGAAATAATTGGGCAAAAGCCGAGTCCGAT	13999
ISU-12-3' TERMINAL (426-1028)	CTGGACACTAAGGGCAGACTTCATCGTTGCCGTTGCCGTGTCATCATAGACAAAGGGGCAAAAGTTGAGCTCGAA	935
LELYSTAD SEQ (13484-14089)	GGCAACCTCGTCACTCAAAACATGTGTTCTTGAAGGGTTAAAGCTGAACCTTTTACAGAGACTTCGGTGA	14073
ISU-12-3' TERMINAL (426-1028)	GGTCACTTATGAGCTCAAAAGAGTTGTGCTTGAATGTTCCGGCGCTTACCCCTGTAAACAGAGTTTCAAGGGA	1009
LELYSTAD SEQ (13484-14089)	CCAAATGGAGCTCTAG-----	14089
ISU-12-3' TERMINAL (426-1028)	ACAAATGGAGTCTCTCTAG	1028

FIG. 8

ISU 12/7a/3' terminal (888 – 1413)	ATTCGACTCG	14132
Lelystad seq (14077 – 14598)	TCCTTAGATG AGTTGTGTCAT TCATAGGACG GGTCCACAAA AGTTCCTCTT	947
	-ATGG-GAGG --GGTAGAG ATTCTTTCGCA GATCCCTATC GCGGCACAAA AGCTCGTCTT	14132
ISU 12/7a/3' terminal (888 – 1413)	GCGCTTTTCT ATTACCTACA GCGGAGTGCAT GATATATGCC CTAAAGGTGA GTCCGGGCGG	1007
Lelystad seq (14077 – 14598)	AGCCTTAGC ATCAATACA CACCTATTAAT GATATACGCC CTAAAGGTGT CACGGGCGCG	14192
ISU 12/7a/3' terminal (888 – 1413)	ACTCTTAGGG CTTGTGCACC TTCTGGTCTT CCTGAATGTCT GCTTTCAGCT TCGGGTACAT	1067
Lelystad seq (14077 – 14598)	ACTCTTGGG CTGTGCACA TCCCTAATATT TCTGAACGTG TCTTTCAGCT TCGGATACAT	14252
ISU 12/7a/3' terminal (888 – 1413)	GACATTCCTG CACTTTCAGA GTACAAATAA GGTGGGCTTC ACTATGGGAG CAGTAGTTGC	1127
Lelystad seq (14077 – 14598)	GACATATCTG CATTTTCAAT CCACCAACCG TGTGGACCTT ACCCTGGGGG GTCCTGTGG-	14311
ISU 12/7a/3' terminal (888 – 1413)	ACTCTTTTTC GGGGTGTACT CAGC--CATTA GAACTTGA ATTTCATCAC CTCCAGATGC	1185
Lelystad seq (14077 – 14598)	-CCTTCTGT GGGGTGTJTTA CAGCTTCACA GAGTATGGA AGTTTATCAC TTCCAGATGC	14370
ISU 12/7a/3' terminal (888 – 1413)	CCTTTGTGCT TGTAGGCGG CAAGTACATT CTGGCCCTG CCCACCAGT TGAAGTGCC	1245
Lelystad seq (14077 – 14598)	AGATTGTGCT GCGTTGGCG GCGATACATT CTGGCCCTG CCCATCAGT AGAAGTGCT	14430
ISU 12/7a/3' terminal (888 – 1413)	GCAGCTTTC ATCCGATTTC GCGAAATGAT AACCAACCAT TTCTGTCTCG CCGTCCCGG	1305
Lelystad seq (14077 – 14598)	GCAGGTCTCC ATTCAATCTC AGCTGTGCT AACCAACCAT AGCTGTGAG AAAGCCGGA	14490
ISU 12/7a/3' terminal (888 – 1413)	TCCACTACG TCAACGGCAC ATTCTTCC GGGTTAAAAA GCCTCGTGT GGTTCGCGA	1365
Lelystad seq (14077 – 14598)	CTACATACG TCAACGGCAC TTTAGTACCA GGAATTCGGA GCCTCGTGT GGTTCGCGA	14550
ISU 12/7a/3' terminal (888 – 1413)	AAAGCTGTTA AAGAGGAGT GGTAAACCTT CTTAATATG CAAAATAA	1413
Lelystad seq (14077 – 14598)	CGAGCTGTTA AAGAGGAGT GGTAAACCTT CTAAAGTATG GCGGTAA	14598

FIG.9

Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	ATGCCCGGTA AAAACCAGAT- GCCCAGAGAA AAAGAAAGT A- CAG ----C ----- AT GCCAAATAC ACCGGCAAGC AGCAGAAAGAG	14632 1434
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TCCCATCGGG AATGCCCAGC CAGTCAATCA ACITGGCCAG TTGCTGGGTG AAGCAAGGGG GATGCCCAGC CAGTCAATCA CCTGTGCCAG ATGCTGGGT-	14681 1483
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CAATCATAAA GTCCACCGC CAGCAACCTA GCGG--A- GG ACAEGCCAAA -AA- CATCAT CGCTACCAA AACCACTCCA GAGCCAAAGC ACCCG---GA	14728 1528
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	AAGAAAA-- ---- -CCTGAGAAG CCACATTTC CCTGGGTGG AAGAAAAATA AGAAGAAAAA CCGCGAGAGAG CCGCATTTC GTCTAGCCAG	14766 1578
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TGAAGATGAC ATCCGCCACC ACCTACCCA CACTGAAAGC TCCGTTCCT TGAAGATGAT GTGAGACATC AGTTTACCCG TAGTGAGCGT CAATTGTGTC	14816 1628
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TCCAATCCAT CCAGACCGGT TTCAATCAAG GCGCAGGAAQ -TCCGTCCCT TGTCGTCAAT CCAGACCGC TTAAATCAAG GCGCTGGGAG TTGCAAG-CCT	14865 1677
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	TTTCATCCAG CCGAAGCTCA GTTTTCAGCT TCAGTTTAGT CTGCCGGTTG GTCAGATTCA GGGAGCAJAA GTTACACTGT GAGTTTAGT TTGCCGTACGC	14915 1727
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	CTCATACAGT GCGCCCTGATT CCGGTGAGTT CTACATCCGC CAGTCAGGT ATCATAGCT GCGCCCTGATC CCGGTGACAG CATCACCC-T CAG-CATGA-	14965 1774
Lelystad seq (14588 – 14974) ISU 12/7a/3' terminal (1403 – 1774)	GCAAGTTAA	14974 1774

FIG.10

ISU 12/7a/3' terminal (1775 – 1938)	TGGGCTGGCA TTCTTGAGGC ATCCAGTGT TTGAATTGGA	1814
Lelystad seq (14975 – 15101)	-----	14976
ISU 12/7a/3' terminal (1775 – 1938)	ACAAATCCGTC GTGAATGGCA CTGATTGACA TTGTCCTCT	1854
Lelystad seq (14975 – 15101)	TGACAGTCAG GTGAATGGGC GCGATTGGC TGTGGCCTCT	15016
ISU 12/7a/3' terminal (1775 – 1938)	AAGTCACCTA TTCAATTAGG GCGACGCTG GCGGGTAACA	1800
Lelystad seq (14975 – 15101)	GAGTCACCTA TTCAATTAGG GCGATGACAT GCGGGTCATTA	15056
ISU 12/7a/3' terminal (1775 – 1938)	TTTAAATTTGG CGAGAACCAC ACCTCCGAAA TTAAAAAAA	1933
Lelystad seq (14975 – 15101)	CTTAATCAGG CAGGAACCAT GTACCCGAAA TTAAAAAAA	15096
ISU 12/7a/3' terminal (1775 – 1938)	AAAAA	1938
Lelystad seq (14975 – 15101)	AAAAA	15101

FIG. 11

1004050 1004050

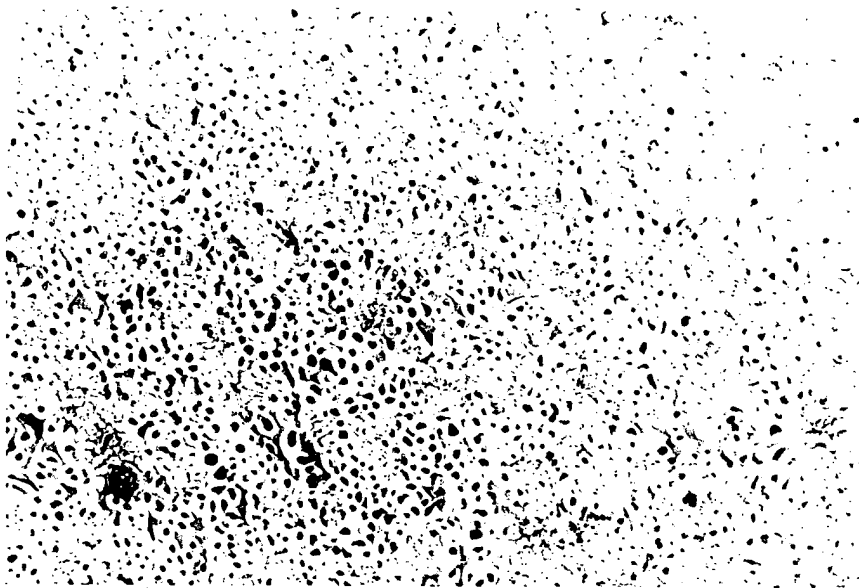


FIG.12

FIG. 13

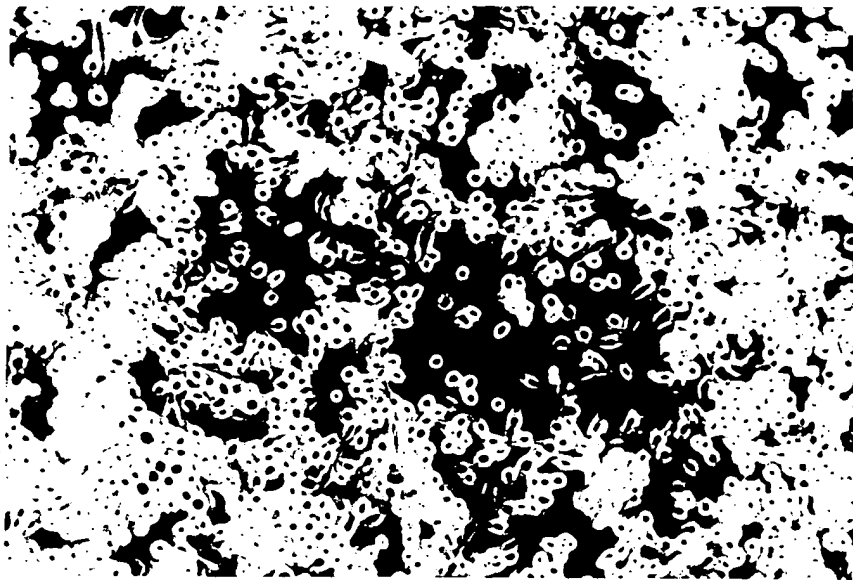


FIG.13



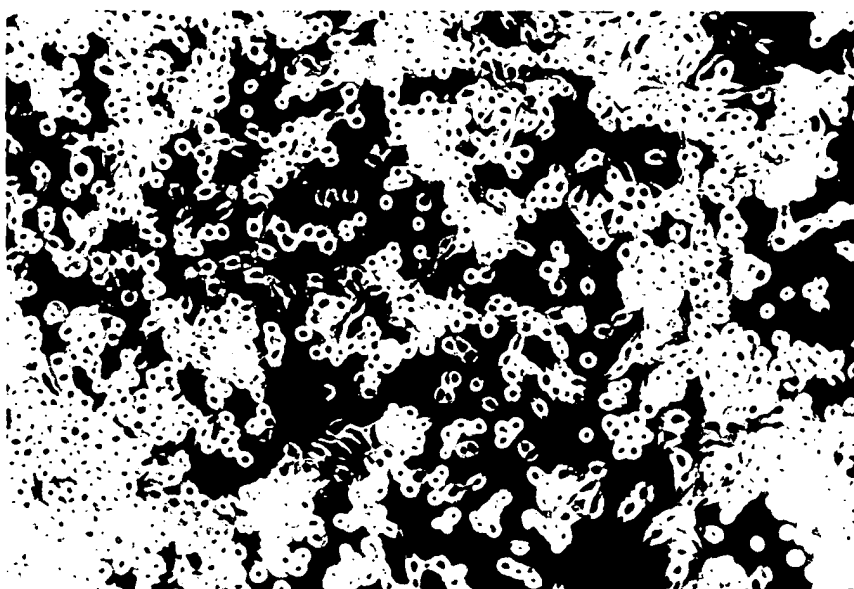


FIG.14

SM E M NP E+M+NP SM

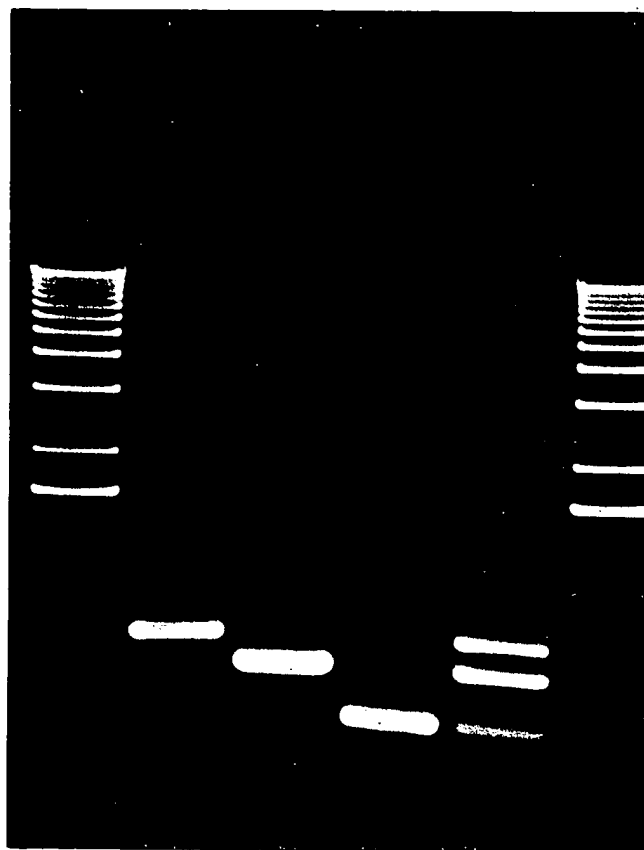


FIG.15

SM pVL1393 E M NP SM



FIG.16

FIG. 17A

VR 2385 GTTGTGCTTGGTAGGGCCGAAGTACATTCTGGCCCCTGGCCACCACGTTGAAAGTGGCCGAGGCTTTCATCCGATTGGGGCAAAATGATACCCACGCAATT 398  
 ISU-1894 ..... 398  
 ISU-22 ..... 398  
 ISU-79 ..... 398  
 ISU-55 .....T.....A..... 398  
 ISU-3927 .....G..... 398  
 LV .....A.....T.GC..T....GCGA.....T.....A.....TC.C...T.A.CT.A.GTC..G....GA...A 395

VR 2385 TGTGCTCCGGGCTCCGGGCTCCACTACGGTCAACGGGCACATTGGTGGCCGGGTTAAAAAGGCTCGTGTGGGGTGGCAGAAAAAGCTGTTAAACAGGGAGTG 498  
 ISU-1894 .....G..... 498  
 ISU-22 .....T.....G..... 498  
 ISU-79 .....G..... 498  
 ISU-55 .....T.....G.....C..... 498  
 ISU-3927 .....T.....G.G.....A.....G..... 498  
 LV C.CT.GA.AAAG....ACTA.AT.A.G.....TC.A.A.A.AC.TCGG.....C...C...A.CG.....GA.... 495

DRF 7 start  
 + 1> \*\*\* DRF 6 stop

VR 2385 GTAACCTTGTAAATATGGCCAAATAACACCGGCA-AGCAGCAGAGAGGAAGAA-----GGGGGATGGCCAGCCAGTCAATCAGCTGTG 582  
 ISU-1894 .....C.....A..... 582  
 ISU-22 .....C.....A..T.. 582  
 ISU-79 .....C.....A..... 582  
 ISU-55 .....A.....A..... 582  
 ISU-3927 .....A.....A..... 582  
 LV .....T.....C.C.G...G.CGG..A.A.--.G.--...A.....AAGTACAGCTCCGAT...A.....A..... 591

FIG. 17B

VR 2385 CCAGATGCTGGGT--AA-GATCATCGCTCACC AAAACCAGTCCAGAGGGCAAGGGACCGGGAAGAAAAAT AAGAAGAAAAACCCGGAGAGCCCAITTC 679  
 ISU-1894 ..... --, -, ..... G, ..... C, ..... T 679  
 ISU-22 ..... C--, -, ..... G, ..., T, ..... I 679  
 ISU-79 ..... --, -, ..... C, G, ..... T, ..... I 679  
 ISU-55 ..... --, -, ..... G, ..... C, ..... I 679  
 ISU-3927 ... A, ..... --, -, ..... C, G, ..... T, ..... I 679  
 LV ..... T, ..... GC, T, ..., A, AGT C, G, ---G, ..., --, -, CCT G, ..., ---, C, ---GCC, A, ..... G, T, ..... A, ..., T 679

VR 2385 CCTCTAGCGACTGAAGATGATGTCAGACATCACCTTACCCCTAGTGAAGCGTCAATTGTTGTCGTGTCATCCAGACCGCCTTAAATCAAGGCCCTGGGA 779  
 ISU-1894 ..... C, ..... G, ..... 779  
 ISU-22 ..... G, ..... 779  
 ISU-79 ..... G, ..... A, T, ..... 779  
 ISU-55 ..... C, T, G, ..., G, ..... A, ..... A, ..... 779  
 ISU-3927 ..... C, ..., C, ..., G, ..... T, ..... G, ..... 779  
 LV ... C, G, TG, ..... CA, C, G, C, ..., C, C, ..., AG, C, ..., A, C, CCG C, CT, CAA, G, ..., G, T, C, ..... A, A, ..... 779

FIG. 17C



VR 2385 DRF6 MESSLDGFCHDSTAPQKLLAFSITYTPWMIYALKVSRGRLGILLVFLNCAFTFGYMTFVHFQSTNKVALIMGAVALLWGVSAIETWKTITSRCR 100  
 ISU-1894 DRF6 .G.....I..... 100  
 ISU-22 DRF6 .G.....I..... 100  
 SIU-55 DRF6 .G.....I..... 100  
 ISU-79 DRF6 .G.....Y.....M..... 100  
 ISU-3927 DRF6 .G.....N.....I.....E..R..... 100  
 LV DRF6 .G-G...N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S..... 99  
 PRRSV-10 DRF6 .G-G...N.PI.A.LV.....I.....S.....Y.....R...L.....FT.S..... 99  
 LDV-C DRF2 .G-G.-E..DATSWY.-IFI...L...IA.S..F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL...I..V..I.TLWKIVDWLV... 96  
 LDV-P DRF2 .G-G.-E..DATSWY.-I.I...L...IA.S..F..T.A.IVNIFI.I..CVS.V.LMYH.-SV..TI..SL...I..V..I.TLWKIVDWLV... 96

VR 2385 DRF6 LCLLGRKYILAPAHVESAGFHP1AANDNH-----AFVRRPGSTIVNGTLVPGKSLVLGGKAVKQGVNLYKY-AK 183  
 ISU-1894 DRF6 .....----- 174  
 ISU-22 DRF6 .....----- 174  
 SIU-55 DRF6 .....----- 174  
 ISU-79 DRF6 .....----- 174  
 ISU-3927 DRF6 .....-----R.....K.....-.. 174  
 LV DRF6 ..C..R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR..R.....-GR 173  
 PRRSV-10 DRF6 .C..R.....L.S.S.SG.R-----YA.K.L.S.....R.....KR..R.....-GR 173  
 LDV-C DRF2 ..F..S...PS..D-----TSDGRQSLTISLTI...K...L..Q..DFOR...K..SK.A..L..VS. 171  
 LDV-P DRF2 ..F..S...PS..D-----TSDGRQSLTISLTI...K...L..Q..DFOR...K..SK.A..L..VS. 171

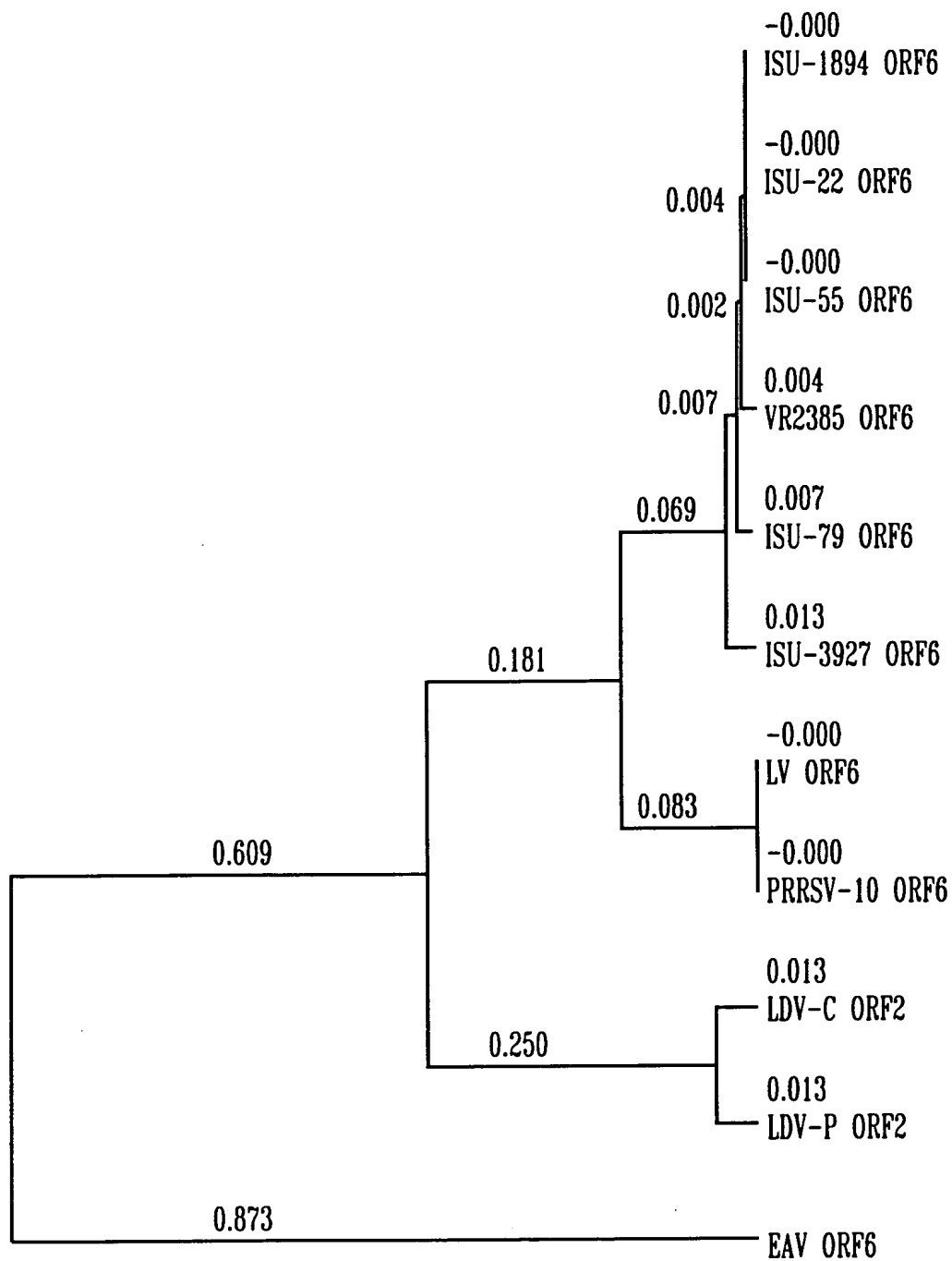
FIG. 184



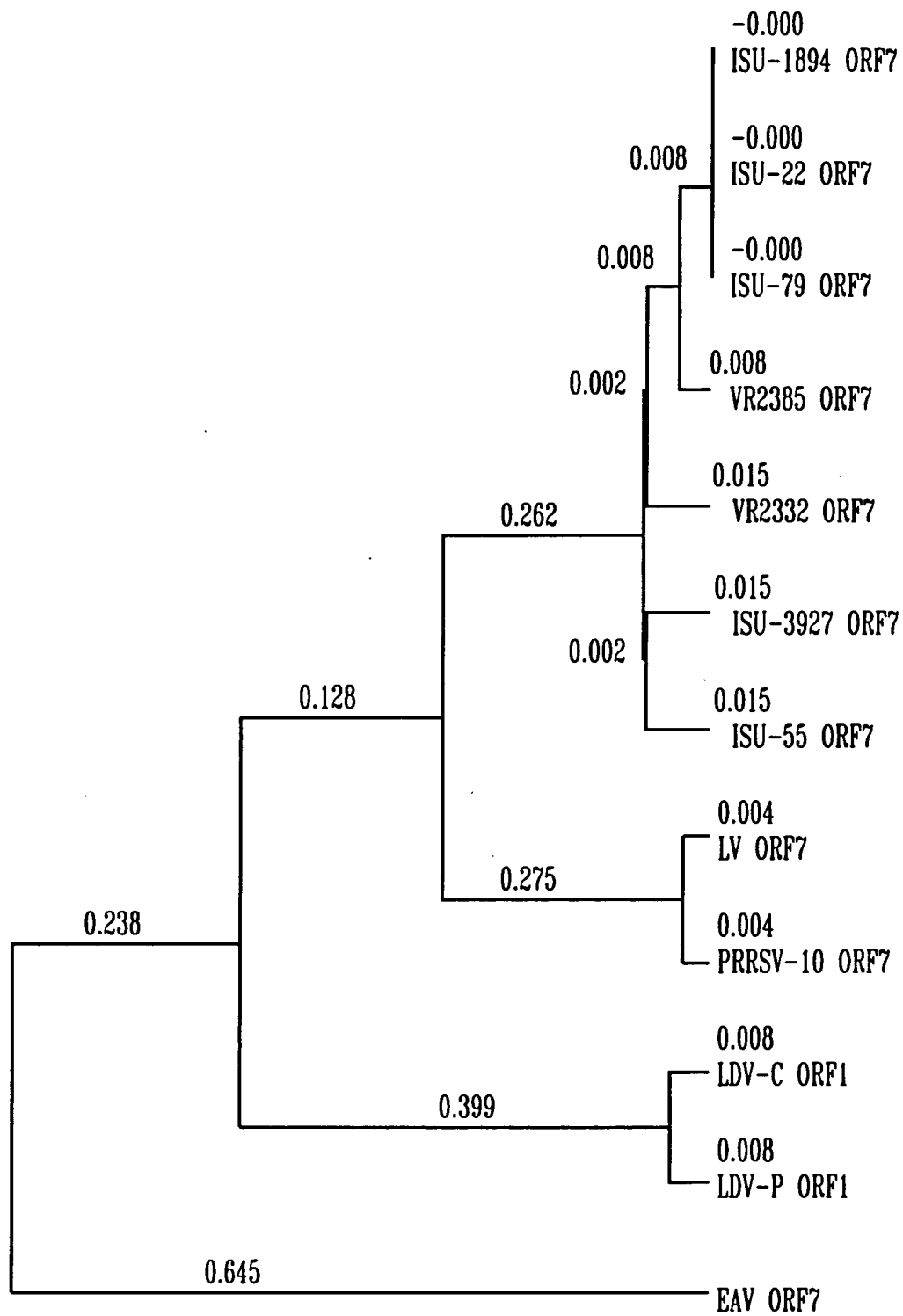
VR 2385 DRF7 MPNNTGKQKQKRRK-----GIDGQPVNQLCQMLGKI1AHQNDNRGKGPGKKNKKKNPEKPHPLATEDDVRRHFTPSERQLCSSIQIAFNQAGAGTCTLS 100  
ISU-1894 DRF7 ...N.....-----Q.....Q.....  
ISU-22 DRF7 ...N.....-----Q.....Q.....  
ISU-79 DRF7 ...N.....-----Q.....Q.....  
ISU-3927 DRF7 ...N.....K.....Q.....Q.....  
ISU-55 DRF7 ...N.....K.....Q.....Q.....SG.....  
VR2332 DRF7 ...N...TEE.....Q.....Q.....  
LV DRF7 ---A..N.SQ..KKSTAPM.N.....L..AM.KS.R.---QPR.GQA..K.....A..I..L.QT..S..Q.....AS.. 93  
PRRSV-10 DRF7 ---A..N.SQ..KKSTAPM.N.....L..AM.KS.R.---QPR.GQA..K.....A..I..L.QT..S..Q.....PS.. 94  
LDV-C DRF1 ..SQ.KK.GGAN-----AN.---.N.LISALLRNAG--N..K.Q.K.-Q.-L..M.GPS.L.VM..N.V.M.R..LV.L...G.Q...V 85  
LDV-P DRF1 ..SQ.KK.SGAN-----AN.---.N.LINALRNAG--N..K.Q.K.-Q.-L..M.GPS.L.VM..N.V.M.R..LV.L...G.Q...V 85  
EAV DRF7 .ASRRSRP.AASF-----RN.R--RRQPTSYNDLLRMFG.-----MRVR.PPAQPTQAI1I.EPG.L..DLNQG..ATLS.NV.RF.MI.H.SL.-A 83  
^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^ ^

VR 2385 DRF7 DSGRISTYVEFSLPTHHTVRLIRVTASP-----SA 134  
ISU-1894 DRF7 ..... 123  
ISU-22 DRF7 ..... 123  
ISU-79 DRF7 ..... 123  
ISU-3927 DRF7 .....P.---. 123  
ISU-55 DRF7 ..... 123  
VR2332 DRF7 ..... 123  
LV DRF7 S..KV.FQ..M..VA.....STASQAGAS 128  
PRRSV-10 DRF7 S..KV.FQ..M..VA.....STASQAGAS 128  
LDV-C DRF1 ...G.NF..S.M...A...NAS.NS----- 115  
LDV-P DRF1 ...G.NF..S.M...A...NAS.NS----- 115  
EAV DRF7 .A.GLT...SW-V..KQIQ.KVAPP.G.----- 110  
^ ^ ^ ^ ^ ^

FIG. 18B



*FIG. 19A*



**FIG. 19B**

+ Start DRF2

100 CCTGAATTGAGATGAAATGGGGTCTATGCAAAAGCCTTTTGGACAAAATTGGCCAACCTTTTGTGGATGCTTTCACGGAGTTCCTGGTGTCATTGTTGAT

200 ATCATTATATTTTGGCCATTTTGTGGCTTCACCATCGCAGGTGGCTGGTGGTCTTTTGTGATCAGATTGGTTTGTCTCCGCGATACTCCGTGGCGGCC

300 CTGCCATTCACTCTGAGCAATTACAGAAAGATCCTATGAGGCCTTTCTCTCTCAGTGCAGGTGGACATTCCCACCCTGGGGAACTAAACATCCTTTTGGGGA

400 TGCTTTGGCACCATAAGGTGTCAACCCTGATTGATGAATGGTGTCCGCTCGAATGGTGTCCGCTGCAATGTACCGCATCATGGAAAAGCAGGACAGGCTGCCTGGAAACAGGT

500 AGTGAGCGAGGCTAGGCTGTCTCGCATTAGTAGTTGGATGTGGTGGCTCATTTTTCAGCATCTTGGCCGCAATTGAAGCCGAGACCTGTAAATATCTGGCC

600 TCTCGGCTGCCCATGCTACACCACCCTGGCGATGACAGGGTCAAAATGTAACCATAGTGTATAATAGTACTTTGAATCAGGTGTTGCTGTTTCCCAACCC

+ Start DRF3

700 CTGTTCCCGGCCAAAGCTTCATGATTTCCAGCAATGGCTAATAGCTGTACATTCCCTCTATATTTCCCTGTTGCAGCTTCCTTTTGTACTCTTTTGTGTTGT

\*\*\* Stop DRF2

800 GCTGTGTTGCGGTTCCAAATGCTACGTACTGTTTGTGTTCCGCTGGTTAGGGGCAATTTTCTTTCGAATCAGGTTGAATTACACGGTGTGCCGC

900 CTTGCCTCACCCGGCAAGCAGCCGAGAGGCTACGAACCCGGCAGGTCCCTTTGGTGCAGGATAGGGCATGATCGATGTGGGAGGACGATCATGATGA

1000 ACTAGGTTTGTGTTGCCGTCTGGCCCTCCAGCGAAGGCCACTTGACCAGTGTCTACGGCTGGTTGGCGTCCCCTGCTTCAGCTATACGGCCCAAGTTC

1100 CATCCCGAGATATTCGGGATAGGGAAATGTAGTTCAGTCTATGTTGACATCAAGCACCAATTCATTTGCGCTGTTTCATGATGGGCAGAACACCACCTTGC

*FIG. 20A*

+ Start DRF4  
 CCCACCATGACAACATTTACGCCGTGCTTCAGACCTATTACCAGCATCAGGTCGACGGGGGCAATTGGTTTCACCTAGAATGGTGCTCCCTTCTTTC 1200  
 CTCCTGGTTGGTTTTAAATGTCCTCTGGTTTCTCAGGGGTTGCCGTGCAAGCCATGTTTCAGTTCGAGTCCTTCAGACATCAAGACCAACACCACCGCAG 1300  
 CCGCAGGGCTTTGCTGTCTCCAGACATCAGTTGCCTTAGGCATCGCAACTCGGCCCTCGAGGCGATTGCGAAAGTCCCTCAGTGGCCGACGGGATAGG 1400  
 GACACCGGTGTATACACTGTCACAGCCAATGTTACCGATGAGAAATTATTGCATTCCCTCTGATCTTCTCATGCTTTCCTTGGCTTTTCTAIGCTTCT 1500  
 GAGATGAGTGAAAAGGGATTTAAGGTGGTATTTGGCAATGTGTCAAGGCATCGTGGCAGTGTGCGTCAACTTCACCAGTTACGTCCAACATGTCAAGGAAT 1600  
 TTACCCACGTTCCCTGGTAGTTGACCAITGTGGGGCTGCTCCATTTCATGACGCCCGAGACCATGAGGTGGGCAACIGTTTTAGCCTGCTTTTTTACCAT 1700  
 \*\*\* Stop DRF4 + Start DRF5  
 TCIGTTGGCAATTTGAATGTTAAGTAIGTTGGGAAATGCTTGACCGGGGCTGTGCTCGCAATTGCTTTTTTATGGTGATCGTGCCGCTTGT 1799

*FIG. 20B*



[illegible]

**FIG. 21A.1**

Consensus	ATGGCTMATMRSTGTRCAYKCYTCYATWTTTCTCTGTGKGCWKCTCTKKTACYYTKTYRTWGTGCTKGGYTKGRRTTCCARYKCTACGYWMTGTT	100
LV DRF3	.....C..CAG..G..CG..T..C..T.....G..TT..A...GT...CT..G..CA..A.....T...C..T..AA.....GCT.....CTA....	100
VR2385 DRF3	.....A..AGC...A..TT..C..T..A.....T..AG..T...TG...TC..T..TG..T.....G...T..G..GG.....ATG.....TAC....	100
Consensus	TTTGGTTTCCRYTGGYMRSGGCAAYWWTCTTCGARCTSACRSISAAYTACACSRTRTGCMYGCCYTYGYYACCMGKCAAGCRGCTCGCMRARGSCT	200
LV DRF3	.....AT...CCCAC.....CACA..A.....G..G..CA..C..C.....CA..A...AT...C..TICT...A..T.....G.....CA..A..G..	200
VR2385 DRF3	.....GC...TTAGG.....TTTT..T.....A..C..GG..G..T.....GG..G...CC...T..CCTC...C..G.....A...-...AG..G..C...	199
Consensus	ACGARCCCGYMGKWMCMKTGGTGCARRATAGGGCATGAYMGRTGTGRGGAGSRVGYCATGATGARYTAGKWWTGTCSRTSCCGTCYGGSYWCKMCA	300
LV DRF3	....G.....TC..TAA..A..G.....AA.....CA..G....A....CGT...C.....GT...-..TTAA...CA..C.....C...GTA..GA..	298
VR2385 DRF3	....A.....CA..GTC..C..T.....GG.....TC..A....G....GAC...T.....AC...GGTT...-GG..G.....T...CCT..TC...	298
Consensus	sRCGAMKSMMACTTGACSRGKMTTAYGCTYGGYTGCKTYYYTGTCCTYWSCYATRCGGCCCARTTCCATCCSGAGWTRTTCGGGATAGGGAATGIGWS	400
LV DRF3	A..--CTCAA.....-GG..TA...T..T...C...T..TTT.....TTC...CG.....A.....G...T..G.....TC	395
VR2385 DRF3	G...AGGCC.....CA..GC...C..C...T...G..CCC.....CAG...TA.....G.....C...A..A.....AG	398
Consensus	KCGMGCTWYGTGACAWSMRRCACCARTTCATTGTGCGYGWKCATGATGGRCSAAYVCMACCKTRYCYMMCSRWSACAACATYTCMGCMKTRYWTSMG	500
LV DRF3	G..C....TC..G...AGCGA.....G.....T..C..AG.....A...C...TT..A...G..AT..TAC..GGAC.....C..C...AT..ATA..GC..	495
VR2385 DRF3	T..A....AT..T...TCAAG.....A.....C..T..TT.....G..G..CA..C...T..GC..CCA..CATG.....T..A...CG..GCT..CA..	498

FIG. 21B



Consensus	RCMTATTACCASCAYCARRTMGACGGGGCAATTGGTTYCAYYTRGAATGGSTGGCKCCMYTCTTTTCYTCYTGGTGGTKYTMAYRTMTCWTGTTTC	600
LV DRF3	G. A. .... C. C. AA. A. .... C. TT. G. .... C. .... G. AC. .... T. C. C. .... GC. C. CA. A. A. ....	595
VR2385 DRF3	A. C. .... G. T. GG. C. .... T. CC. A. .... G. .... T. CT. .... C. T. .... T. A. TG. C. T. ....	598
Consensus	TSAGGCGTTCCGCTGYAAGCCMTGTTTCWSKWCGRMRTCTWTCAGAYATYRAGACCAACACACACCGCRGCKGCMGGYTTYRYKGTCTCTYCARGACATCART	700
LV DRF3	. G. .... T. .... C. .... TCGA. CA. A. .... T. TG. .... G. .... T. C. T. CATG. .... T. G. .... A.	695
VR2385 DRF3	. C. .... C. .... A. .... AGTT. AG. . T. .... C. CA. .... C. .... A. G. A. C. TGCT. .... C. A. .... G.	698
Consensus	TGYTYMGRCMTCACGGSRWCTCRGCAGCKCAWGAGRMRAITTCCTTCGSAAGTCGYCYCARTGYCGYGAMGCGWVRGTACTCCCCAGTACATCACGA	800
LV DRF3	. . TT. CC. A. C. .... GGT. . . A. .... G. A. . . AAA. .... G. .... T. C. A. T. . T. A. C. TCG. ....	795
VR2385 DRF3	. . CC. TA. G. A. . ---. CAA. . . G. . --. T. -T. . . GCG. -----. C. T. G. C. C- C. G. ATA. -----	765
Consensus	TAA	803
LV DRF3	. . .	798
VR2385 DRF3	----	765

FIG. 21B.1



Consensus	M. WG. C. . K. . . . . L. . . . . W. . . . . L. . . . . P. CL. SPSQ. G. WSF. S. WFAPR. SVRALPFTL. NYRRSYE. . L. . C. . . D. P. . . . . KH	100
LV DRF2	. Q. . H. GV. SASCSWTPS. SSSLV. LI-----PF. . ---. Y. . G. . . . D. Y. . . F. E. . . . . P. . . . . GL. PN. RP. V. QFAV. .	90
VR2385 DRF2	. K. . L. . --. ----AFLTK. AN-FL. MLSSSWCP. LI. . YFW. F. . A. . . . V. W. . . A. D. . . . . Y. . . . . S. . . . . AF. SQ. QV. I. TWGT. .	93
Consensus	PLGM. WH. . VS. LIDEMVSR. Y. . ME. . GQAAWKQVV. EATL. . . S. LD. V. HFQHLAA. EA. . C. . L. SRL. ML. . L. . . . . NV. . . . . YN. TL. . V. . .	200
LV DRF2	. . . . F. . MR. . H. . . . . I. QT. . HS. . . . . G. . . . . TKL. G. . I. T. . . . . V. . DS. RF. S. . . V. . KN. AV--G. . SLQ. . T. . DR. ELI	188
VR2385 DRF2	. . . . L. . HK. . T. . . . . M. RI. . KA. . . . . S. . . . . SRI. S. . V. A. . . . . I. . ET. KY. A. . . P. . HH. RMTGS. . TIV. . S. . NQ. FAV	193
Consensus	FPTPG. RPKL. DF. QWLI. VH. SIFSSVA. S. TLF. VLWLR. P. LR. VFGF. W. . A. . . . .	264
LV DRF2	. . . . . T. . . . T. . R. . . . S. . A. . . . . S. V. . . I. . . . . I. A. . Y. . . . H. PT. ---THSS	249
VR2385 DRF2	. . . . . S. . . . H. . Q. . . . A. . S. . . . . A. C. . . V. . . . . V. M. . T. . . . R. LG. IFLNSR-	257

FIG. 22A

Consensus	MA, C, . . . . .	FLC, . . . . .	Y, . . . . .	A, . . . . .	S, . . . . .	T, CFWFPL, . . . . .	GN, SFELT, NYT, C, PC, T, QAA, . . . . .	EPGR, . . . . .	WC, IGHDRC, E, DHDEL, . . . . .	PSG, . . . . .	100
LV DRF3,	. . . . .	HQ, ARFHF, . . . . .	GFIC, LVHS, LASN, SS, L, . . . . .	AH, T, . . . . .	I, . . . . .	I, M, S, S, . . . . .	RQRL, . . . . .	NM, K, . . . . .	E, R, . . . . .	LMSI, . . . . .	YDN 100
VR2385 DRF3,	. . . . .	NS, TFLYI, . . . . .	CSFL, SFCC, VVAG, NA, Y, . . . . .	VR, F, . . . . .	V, . . . . .	V, P, L, R, . . . . .	AEAY, . . . . .	SL, R, . . . . .	G, D, . . . . .	GFVV, . . . . .	LSS 100
Consensus	. . . . .	L, . . . . .	YAWLA, LSFSY, AQFHPE, FGIGNVSRV, VD, . . . . .	HQFICA, HDG, N, T, . . . . .	NISA, . . . . .	YY, HQ, DGGNWFHLEW, RP, FSSWLVLN, SWFL					200
LV DRF3,	. . . . .	L-K, EGY, . . . . .	F, . . . . .	A, . . . . .	L, . . . . .	F, KR, . . . . .	E, H, S, VSTGH, . . . . .	LYAA, H, I, . . . . .	L, . . . . .	I, . . . . .	199
VR2385 DRF3,	. . . . .	EGH, TSA, . . . . .	S, . . . . .	T, . . . . .	I, . . . . .	Y, IK, . . . . .	V, . . . . .	Q, T, LPHHD, . . . . .	VLQT, Q, V, . . . . .	V, . . . . .	200
Consensus	. . . . .	RRSP, S, VS, R, . . . . .	Q, . . . . .	RPT, P, . . . . .	S, . . . . .	TS, . . . . .	L, . . . . .	R, F, . . . . .	K, S, . . . . .		266
LV DRF3,	. . . . .	. . . . .	V, P, . . . . .	R, IY, IL, . . . . .	R, RLPVSW, FR, . . . . .	IVSD, TGSQQRK, K, PSESRPNWV, P, VLPSTSR					265
VR2385 DRF3,	. . . . .	. . . . .	A, H, . . . . .	V, VF, TS, . . . . .	P, QRQALL, SK, . . . . .	V--A, GIATRPL, R, A-----, - , LSAARR-					255

## FIG. 22B

Consensus	M, A, . . . . .	LF, L, G, . . . . .	VS, AFACKPCFS, . . . . .	LSDI, TINTAAAGF, VLQDI, C, R, . . . . .	A, E, I, . . . . .	K, . . . . .	QCR, A, GTP, YIT, TANVTDE, YL, . . . . .	DL	100					
LV DRF4,	. . . . .	A, AT, . . . . .	F, A, AQHIM, . . . . .	E, . . . . .	TH, . . . . .	E, . . . . .	M, . . . . .	N, F, PHGVSA, Q, K, SFG, SS, . . . . .	E, V, . . . . .	Q, . . . . .	I, . . . . .	S, . . . . .	YNA, . . . . .	100
VR2385 DRF4,	. . . . .	G, SL, . . . . .	L, V, FKCLL, . . . . .	Q, . . . . .	SS, . . . . .	K, . . . . .	A, . . . . .	S, L, HR--NS, S, A, R-- , VP, . . . . .	T, I, . . . . .	V, . . . . .	V, . . . . .	N, . . . . .	HSS, . . . . .	96
Consensus	. . . . .	LMLS, CLFYASEMSEKGFKV, FGNVSG, V, . . . . .	CVNFT, YV, HV, . . . . .	TQ, . . . . .	V, . . . . .	RLHF, TP, MRWAT, . . . . .	ACLF, ILLAI, . . . . .							184
LV DRF4,	. . . . .	. . . . .	A, . . . . .	. . . . .	I, . . . . .	V, SA, . . . . .	D, A, . . . . .	TQH, QHHL, IDHI, . . . . .	L, . . . . .	SA, . . . . .	TI, . . . . .	A, . . . . .		183
VR2385 DRF4,	. . . . .	. . . . .	S, . . . . .	. . . . .	V, . . . . .	I, AV, . . . . .	S, Q, KEF, . . . . .	RSLV, DH-V, . . . . .	M, . . . . .	ET, . . . . .	VL, . . . . .	T, . . . . .		179

## FIG. 22C

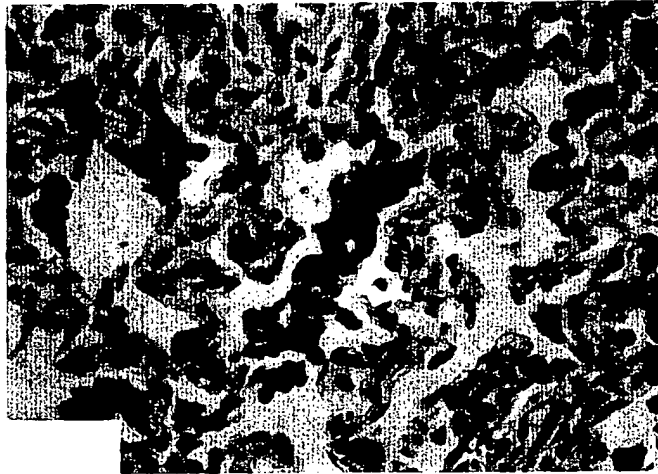


FIG.23

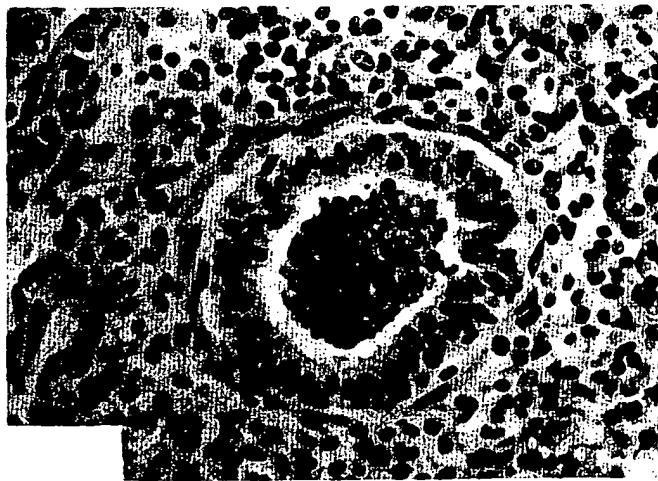


FIG.24

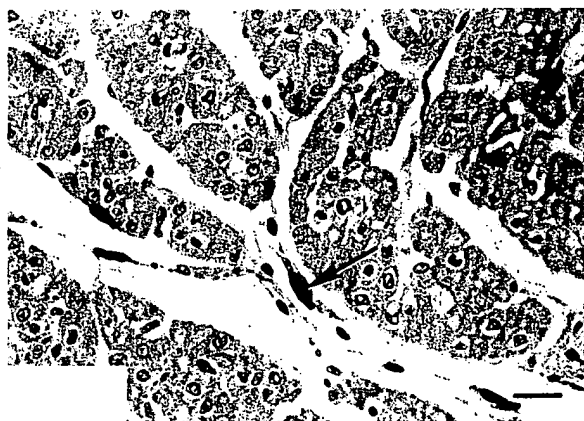


FIG.25

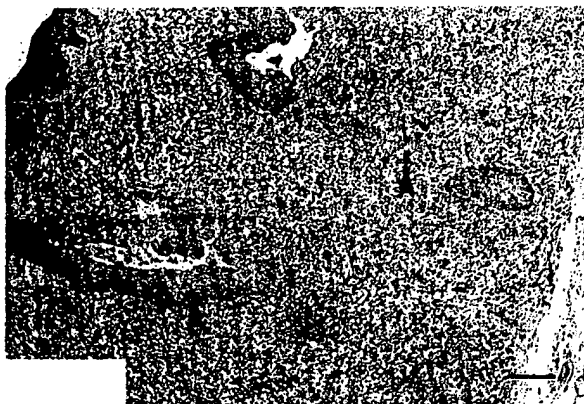


FIG.26

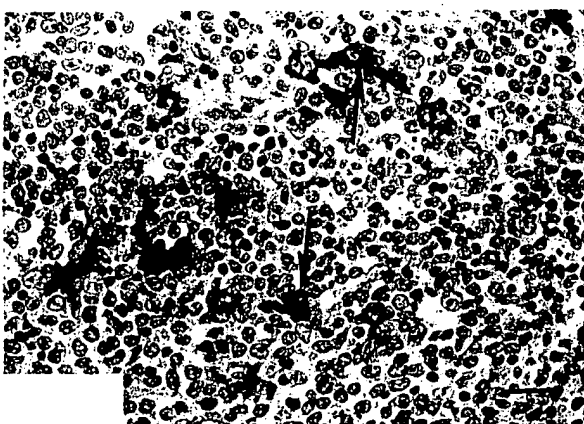
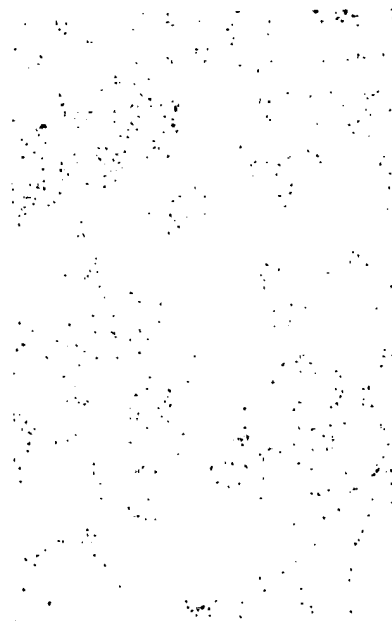
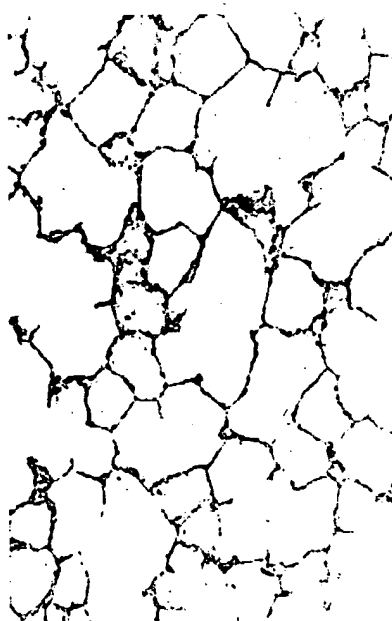


FIG.27

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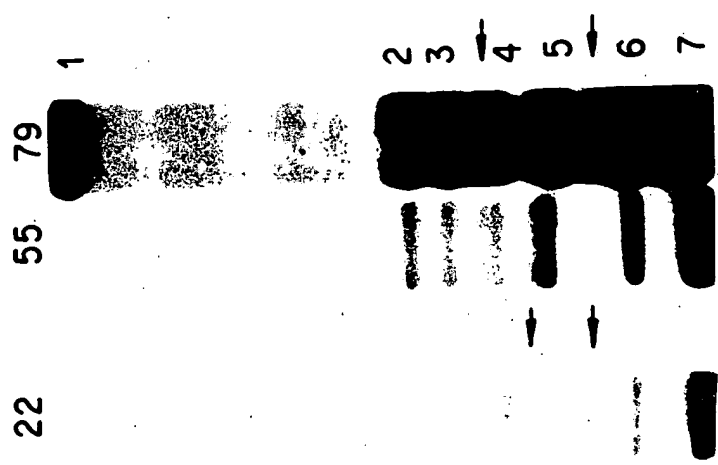


FIG. 30A

1

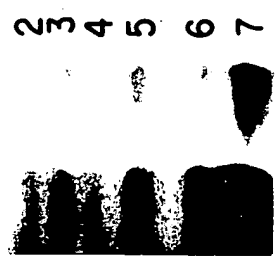


FIG. 30B